Appendix

Pending Claims

1. A method of identifying subjects at risk of developing Crohn's disease comprising:

a) providing

i) nucleic acid from a subject, wherein said nucleic acid comprises a Nod2 gene; and

b) detecting the presence or absence of one or more variations in said Nod2 gene.

2. The method of Claim 1, further comprising step c) determining if said subject is at risk of developing Crohn's diseased based on the presence or absence of said one or more variations.

3. The method of Claim 2, wherein said determining of step c) comprises determining a genotype relative risk for said subject.

4. The method of Claim 2, wherein said determining of step c) comprises determining a population attributable risk for said subject.

5. The method of claim 1, wherein said variation is a mutation.

6. The method of Claim 1, wherein said variation in a polymorphism.

7. The method of claim 1, wherein said variation results in increased NF- B activation.

8. The method of Claim 5, wherein said mutation is a cytosine residue insertion.

9. The method of Claim 5, wherein said mutation causes a deletion of at least one LRR repeat of Nod2.

11. The method of Claim 1, wherein said detecting in step (b) is accomplished by hybridization analysis.

12. The method of Claim 1, wherein said detecting in step (b) comprises comparing the sequence of said nucleic acid to the sequence of a wild-type Nod2 nucleic acid.

24. A computer implemented method of determining a patient's risk of developing Crohn's disease comprising:

a) providing:

i) nucleic acid from a patient, wherein said nucleic acid comprises a Nod2 gene; and

ii) a computer comprising software for the prediction of a patient's risk of developing Crohn's disease; and

b) detecting the presence of one or more variations in said patient's Nod2 gene to generate genetic variation information;

c) entering said genetic variation information into said computer; and

d) calculating said patient's risk with said software.

25. The method of claim 24, further comprising step e) displaying said patient's risk.

26. The method of Claim 24, wherein said risk comprises a genotype relative risk.

27. The method of Claim 24, wherein said risk comprises a population attributable risk.

28. The method of Claim 24, wherein said variation is a polymorphism.

29. The method of Claim 24, wherein said variation in a mutation.

30. The method of Claim 29, wherein said mutation is a cytosine residue insertion.

31. The method of Claim 30, wherein said mutation causes a deletion of at least one LRR repeat of Nod2.

33. The method of Claim 24, wherein said detecting in step (b) comprises comparing the sequence of said nucleic acid to the sequence of a wild-type Nod2 nucleic acid.